What is Claimed is:

1. A process for marking biological samples used in subsequent nucleic acid analysis comprising:

collecting known biological samples;

introducing at least one fragment of deoxyribonucleic acid (DNA) of known length and sequence into the known biological samples.

2. The process for marking biological samples used in subsequent nucleic acid analysis of claim 1, where introducing at least one fragment of DNA further comprises:

providing the DNA fragment as an insert within a plasmid host that allows amplification in *E. coli*.

3. The process for marking biological samples used in subsequent nucleic acid analysis of claim 1, where introducing at least one fragment of DNA further comprises:

providing the DNA fragment as a linear fragment.

4. The process for marking biological samples used in subsequent nucleic acid analysis of claim 1, where introducing at least one fragment of DNA further comprises:

inserting the DNA fragment into a plasmid vector.

5. The process for marking biological samples used in subsequent nucleic acid analysis of claim 4, further comprising:

identifying the DNA fragment through the presence of a first polymerase chain reaction primer and a second polymerase chain reaction primer.

6. The process for marking biological samples used in subsequent nucleic acid analysis of claim 1, where the known length of the DNA fragment complies with a protocol and where the protocol is selected from the group of protocols consisting of (1) a length of DNA which provides PCR product(s) of known lengths when used with appropriate oligonucleotide primers as known in the art, in a PCR reaction in conjunction with short tandem repeats analysis, (2) a length of DNA which provides PCR product(s) of known lengths when used with appropriate oligonucletide primers as known in the art, in a PCR reaction in conjunction with variable numbers of tandem repeats analysis, (3) a length of DNA which can be detected with defined nucleic acid probes when used in restriction fragment length polymorphisms, and (4) a

length of DNA which generates a unique known DNA sequence when used with the appropriate oligonucleotide sequencing primer(s) as known in the art with mitochondrial sequencing.

7. The process for marking biological samples used in subsequent nucleic acid analysis of claim 6 further comprising:

administering to the DNA fragment primers complementary to its two ends.

8. The process for marking biological samples used in subsequent nucleic acid analysis of claim 6 where the DNA fragment has binding sites for two different primers.

9. The process for marking biological samples used in subsequent nucleic acid analysis of claim 6 where a first DNA fragment is inserted into a first plasmid vector and a second DNA fragment is inserted into a second plasmid vector.

10. The process for marking biological samples used in subsequent nucleic acid analysis of claim 9, where the first DNA fragment and the second DNA fragment each have binding sites for two different primers.

11. The process for marking biological samples used in subsequent nucleic acid analysis of claim 6, where the DNA fragment has at least one attribute selected from the list of attributes consisting of (1) the DNA fragment has a stability comparable to the shelf life of biological specimens, (2) the DNA fragment in conjunction with primers used in the addition thereof does not interfere with the subsequent analysis of the known biological sample, (3) the DNA fragment in conjunction with primers used in the addition thereof does not produce any polymerase chain reaction products, restriction fragments, bands detected by hybridization analysis, or DNA sequence other than expected for the added DNA fragment, (4) the DNA fragment is compatible with, and stable through, standard DNA preparation procedures as known in the art, (5) the concentration of the DNA fragment is of a predetermined amount such that it will be present in molar ratios similar to those of the analysis targets in the known biological samples after preparation of the sample for analysis and (6) the DNA fragment, or products generated from the DNA fragment, is compatible with at least one of DNA hybridization analysis, agarose gel electrophoresis, polyacrylamide gel electrophoresis, capillary electrophoresis, or matrix assisted laser desorption ionization time-of-flight mass spectrometry.

12. The process for marking biological samples used in subsequent nucleic acid

analysis of claim 11, where the DNA fragment is added to a collection vessel.

13. A process for marking biological samples used in subsequent nucleic acid analysis comprising:

introducing at least one fragment of deoxyribonucleic acid (DNA) of known length and sequence into a collection vessel;

collecting known biological samples;

adding the known biological samples to the collection vessel to obtain a modified biological sample;

extracting the DNA from the modified sample to obtain extracted DNA;

providing primers complementary to the extracted DNA to obtain a resulting sample;

analyzing the resulting sample using an assay technique selected from the list of assay techniques consisting of polymerase chain reaction-based analysis of short tandem repeats; polymerase chain reaction-based analysis of variable numbers of tandem repeats; DNA hybridization analysis of restriction fragment length polymorphisms; and the sequencing of mitochondrial DNA.

14. The process for marking biological samples used in subsequent nucleic acid analysis of claim 13, further comprising:

producing a polymerase chain reaction product of defined length using a single primer set with a single fragment of DNA.

15. The process for marking biological samples used in subsequent nucleic acid analysis of claim 13, further comprising:

producing fragments of differing sizes in separate polymerase chain reactions using multiple primer sets with a single fragment of DNA.

16. The process for marking biological samples used in subsequent nucleic acid analysis of claim 13, further comprising:

producing multiple fragments in a polymerase chain reaction using a single primer set with multiple DNA fragments.

17. The process for marking biological samples used in subsequent nucleic acid analysis of claim 13, further comprising:

producing multiple fragments in a polymerase chain reaction using multiple primer sets with multiple DNA fragments.

18. The process for marking biological samples used in subsequent nucleic acid analysis of claim 13, where the primers are supplied as components of assay kits.